

SEQUENCE LISTING:

(1) GENERAL INFORMATION:

(i) APPLICANT: DUARTE CANO, C. A.  
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(ii) TITLE OF INVENTION: System for the expression of heterologous antigens as fusion proteins.

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lackenbach Siegel Marzullo Aronson & Greenspan  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).  
(B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).  
(C) OPERATING SYSTEM: Windows 95.  
(D) SOFTWARE: Word Perfect 5.0 for Windows 95.

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/930,917  
(B) FILING DATE: 16-Sep-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/CU97/00001  
(B) FILING DATE: 17-Jan-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: HENRY A. MARZULLO, JR.  
(B) REGISTRATION NUMBER: 20,910

(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:  
(A) NAME/KEY: 1573  
(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
TTCCATGGTA GATAAAAGAA TGGCTTTAG

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1575  
(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTCTAGATC CAAAGTAATC AGGGTATCG

29

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: Primer 2192

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 120 amino acids of the

recombinant protein of *Neisseria meningitidis* P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
GGCGGTTCTG CCGATTAAGG ATCCGA

26

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Fragment amplified by PCR

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Fragment derived from the first 47 amino acids of the recombinant protein of Neisseria meningitidis P64K, containing a Ncol site at the position 3 to 8 and a XbaI site at the position 139 to 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCCATGGTA GATAAAAGAA TGGCTTAGT TGAATTGAAA GTGCCCGACA  
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AAACGTGGGC GACACTATTG  
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA  
146

(2) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

ORGANISM: Neisseria meningitidis  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Stabilizer derived from the first 47 amino acids of the recombinant protein of Neisseria meningitidis P64K, containing the following changes: L2 V2; E45 D45; T46 L46; D47 E47.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
1 5 10 15  
Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
20 25 30  
Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu  
35 40 45

(2) INFORMATION FOR SEQ. ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :  
CTAGATTGATATCAG

16

(2) INFORMATION FOR SEQ. ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

GATCCTGATA TCAAAT

16

(2) INFORMATION FOR SEQ. ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1
- (C) INDIVIDUAL ISOLATE: LR150

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation LR150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr

1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 10:

(A) SEQUENCE CHARACTERISTICS:

- (B) LENGTH: 15 Amino acid residues
- (C) TYPE: Amino acid
- (D) STRANDEDNESS: Unknown
- (E) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: JY1

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation JY1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr

1 5 10

15

(2) INFORMATION FOR SEQ. ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: RF

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala Thr

1 5 10

15

(2) INFORMATION FOR SEQ. ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.  
(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: MN

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation MN.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: BRVA

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the

VIH-1, isolation BRVA.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
Arg Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1
- (C) INDIVIDUAL ISOLATE: IIIB

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the  
VIH-1, isolation IIIB.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
1 5 10 15

**(2) INFORMATION FOR SEQ. ID NO: 15:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 15 Amino acid residues.
- (B) TYPE: Amino acid.
- (C) STRANDEDNESS: Unknown.
- (D) TOPOLOGY: Unknown.

**(ii) MOLECULE TYPE:** Peptide

**(iii) HYPOTHETICAL:** Yes

**(iv) ANTI-SENSE:** No

**(v) FRAGMENT TYPE:** Internal fragment

**(vi) ORIGINAL SOURCE:**

- (A) ORGANISM: VIH-1

**(ix) FEATURE:**

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 7 within the multiepitopic polypeptide (MEP) TAB13.

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:**

Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly  
1 5 10 15

**(2) INFORMATION FOR SEQ. ID NO: 16:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 15 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

**(ii) MOLECULE TYPE:** Peptide

**(iii) HYPOTHETICAL:** Yes

**(iv) ANTI-SENSE:** No

**(v) FRAGMENT TYPE:** Internal fragment

**(vi) ORIGINAL SOURCE:**

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 8 within the multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Arg Leu Tyr Thr Thr

1 5 10

15

(2) INFORMATION FOR SEQ. ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Flexible spacer separating epitopes V3 in the MEP  
TAB3, TAB4,  
TAB9 and TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala Gly Gly Gly Ala

1 5

(2) INFORMATION FOR SEQ. ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB4.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu  
1 5 10 15  
His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile  
20 25 30  
Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Ala Arg Gln  
35 40 45  
Ser Thr Pro Ile Gly Leu Gly Ala Leu Tyr Thr Thr Ala Gly Gly  
50 55 60  
Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala  
65 70 75 80  
Thr Ala Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg  
85 90 95  
Ala Phe Tyr Thr Thr Ala Gly Gly Ala Arg Lys Arg Ile Thr Met  
100 105 110  
Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Ala Ser Ile  
115 120 125  
Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
130 135 140

(2) INFORMATION FOR SEQ. ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB9.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser  
35 40 45  
Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly  
50 55 60  
Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr  
65 70 75 80  
Thr Thr Ala Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly  
85 90 95  
Arg Val Ile Tyr Ala Thr Ala Gly Gly Ala Arg Lys Arg Ile His  
100 105 110  
Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg  
115 120 125  
Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly  
130 135 140  
Gly Gly Ala Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val  
145 150 155 160  
Thr Ile

(2) INFORMATION FOR SEQ. ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment.

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1	5	10	15	
Gly	Gly	His	Glu	
		Asn	Asn	
Val		Val	Asp	
		Ile	Ile	
		Ala	Val	
			Glu	
			Val	
			Asn	
			Val	
			Gly	
20		25	30	
Asp	Thr	Ile	Ala	
		Val	Val	
		Asp	Asp	
		Thr	Leu	
		Ile	Thr	
		Leu	Asp	
			Leu	
			Asp	
			Ser	
35		40	45	
Arg	Gly	Ile	Arg	
		Ile	Gly	
		Pro	Gly	
		Arg	Ala	
		Ile	Leu	
		Ala	Thr	
			Ala	
			Gly	
50		55	60	
Gly	Gly	Ala	Arg	
		Gln	Ser	
		Thr	Pro	
		Ile	Gly	
		Leu	Gly	
		Gln	Ala	
			Leu	
			Tyr	
65		70	75	80
Thr	Thr	Ala	Gly	Gly
		Gly	Gly	Ala
		Arg	Lys	Ser
		Ile	Thr	Lys
			Gly	Pro
				Gly
85		90	95	
Arg	Val	Ile	Tyr	Ala
		Thr	Ala	Gly
			Gly	Gly
			Ala	Arg
			Lys	Arg
			Ile	His
100		105	110	
Ile	Gly	Pro	Gly	Arg
		Ala	Phe	Tyr
			Thr	Thr
			Ala	Gly
			Gly	Gly
			Ala	Arg
115		120	125	
Lys	Arg	Ile	Thr	Met
		Gly	Pro	Gly
			Arg	Val
			Tyr	Tyr
			Tyr	Thr
			Ala	Gly
130		135	140	
Gly	Gly	Ala	Arg	Gln
			Thr	Arg
			Ser	Ile
			Gly	Gly
			Gln	Ala
				Leu
145		150	155	160
Thr	Thr	Ala	Gly	Gly
			Gly	Ala
			Arg	Thr
			Ile	Ser
			Ile	Ile
			Gly	Pro
165		170	175	
Val	Phe	Tyr	Arg	Thr
			Gly	Ala
			Gly	Gly
			Ala	Ser
			Ile	Arg
180		185	190	
Arg	Gly	Pro	Gly	Arg
		Ala	Phe	Val
			Thr	Ile
195		200		

(2) INFORMATION FOR SEQ. ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

OTHER INFORMATION: Codifies for epitopes V3 linked by the spacer of SEQ ID NO: 17: in the  
MEP TAB 19.  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTAGACTCG AGAGGCATTC GTATCGGCC AGGTCGCGCA  
ATTTTAGCAA CAGCTGGCGG 60

TGGCGCACGT CAATCTACCC CTATTGGTTT AGGTCAGGCT  
CTGTATACGA CTGCCGGCGG 120

TGGTGCAGCGC AAAAGTATCA CCAAGGGTCC AGGCCGCGTC  
ATTTACGCCA CCGCGGGCGG 180

CGGTGCCCGT AAGCGTATCC ACATTGGCCC AGGCCGTGCA  
TTCTATACTA CAGCAGGTGG 240

TGGCGCACGT AAACGCATCA CTATGGGTCC TGGTCGCGTC  
TATTACACGA CCGCTGGCGG 300

CGGTGCTAGC ATTCGCATCC AACGCGGCCCTGGTCGTGCA  
TTTGTGACCA TATGATAACG 360

CGGGATCC 368

## SEQUENCE LISTING

SEQUENCE IDENTIFICATION NO.: 1

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: protein fragment.

PROPERTIES: First 47 amino acids of the recombinant protein P64k of *N. meningitidis*.

MLDKRMALVELKVPDIGGHENVNDIIAVEVNVGDTIAVDDTLITLETD 44

SEQUENCE IDENTIFICATION NO.: 2

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 5' No. 1573 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTCCATGGTAGATAAAAGAATGGCTTAG 29

SEQUENCE IDENTIFICATION NO.: 3

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 1575 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTCTAGATCCAAAGTAATCAGGGTATCG 29

SEQUENCE IDENTIFICATION NO.: 4

SEQUENCE TYPE: Nucleotide

LENGTH: 26 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 2192 for PCR amplification of the first 120 amino acids from the P64k antigen of *N. meningitidis*.

GGCGGTTCTGCCGATTAAGGATCCGA 26

SEQUENCE IDENTIFICATION NO.: 5

SEQUENCE TYPE: Nucleotide

LENGTH: 146 base pairs

MOLECULE TYPE: PCR amplified fragment

PROPERTIES: Derived fragment from the first 47 amino acids of the P64k antigen of *N. meningitidis*. Restriction sites Ncol (positions 3 to 8) and XbaI (positions 139 to 144) are introduced by PCR, which provoke changes in the nucleotide sequence of this fragment.

TTCCATGGTAGATAAAAGAATGGCTTAGTTGAATTGAAAGTGCCGACATTGGCGGACA 60  
CGAAAATGTAGATATTATCGCGGTTGAAGTAAACGTGGCGACACTATTGCTGTGGACGA 120  
TACCCCTGATTACTTGGATCTAGAAA 146

SEQUENCE IDENTIFICATION NO.: 6

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: stabiliser fragment derived from the first 47 amino acids of the P64k antigen of *N. meningitidis*.

PROPERTIES: This fragment has the following changes with respect to the P64k.  
L2→V2; E45→D45; T46→L46; D47→E47

MVDKRMALVELKVPDIGGHENVDIIAVEVNVDTIAVDDTLITLDLE 47

SEQUENCE IDENTIFICATION NO.: 7

SEQUENCE TYPE: Nucleotide

LENGTH: 16 bases

MOLECULE TYPE: Synthetic oligonucleotide

CTAGATTGATATCAG 16

SEQUENCE IDENTIFICATION NO.: 8

SEQUENCE TYPE: Nucleotide

LENGTH: 16 bases

MOLECULE TYPE: Synthetic oligonucleotide

GATCCTGATATCAAAT 16

SEQUENCE IDENTIFICATION NO.: 9

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1.  
LR150 isolate.

SRGIRIGPGRAILAT 15

SEQUENCE IDENTIFICATION NO.: 10

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, JY1 isolate.

RQSTPIGLGQALYTT

15

SEQUENCE IDENTIFICATION NO.: 11

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, RF isolate.

RKSITKGPGRVIYAT

15

SEQUENCE IDENTIFICATION NO.: 12

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, MN isolate.

RKRIHIGPGRFYTT

15

SEQUENCE IDENTIFICATION NO.: 13

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, BRVA isolate.

RKRITMGPGRVYYTT

15

SEQUENCE IDENTIFICATION NO.: 14

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, IIIB isolate.

SIRIQRGPGRAFVTI

15

SEQUENCE IDENTIFICATION NO.: 15

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: Consensus sequence of the central region of the V3 loop from the gp120 protein of different HIV-1 isolates, position 7 within the MEP TAB13.

TSITIGPGQVFYRTG

15

SEQUENCE IDENTIFICATION NO.: 16

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: Consensus sequence of the central region of the V3 loop from the gp120 protein of different HIV-1 isolates, position 8 within the MEP TAB13.

RQRTSIGQGQALYTT

15

SEQUENCE IDENTIFICATION NO.: 17

SEQUENCE TYPE: amino acid

LENGTH: 5 amino acids

MOLECULE TYPE: flexible linker that divides the V3 epitopes in the MEP TAB3, TAB4, TAB9 and TAB13.

AGGGA

5

SEQUENCE IDENTIFICATION NO.: 18

SEQUENCE TYPE: amino acid

LENGTH: 141 amino acids

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB4.

MAPTSSSTAQTQLQLEHLLLQIFLSRGIRIGPGRAILATAGGGARQSTPIGLGGALYT 60

TAGGGARKSITKGPGRVYIATAGGGARKRIHIGPGRAFYTTAGGGARKRITMGPGRVYYT 120

TAGGGASIRIQRGPGRAFVTI 141

SEQUENCE IDENTIFICATION NO.: 19

SEQUENCE TYPE: amino acid

LENGTH: 162 amino acids

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB9.

MVDKRMALVELKVPDIGGHENVDIIAVEVNVDIATVDDTLITLDLDSRGIRIGPGRAIL 60  
ATAGGGARQSTPIGLGGALYTTAGGGARKSITKGPGRVYATAGGGARKRIHIGPGRFY 120  
TTAGGGARKRITMGPGRVYYTTAGGGASIRIQRGPGRAFVTI 162

SEQUENCE IDENTIFICATION NO.: 20

SEQUENCE TYPE: amino acid

LENGTH: 202 amino acids

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB13.

MVDKRMALVELKVPDIGGHENVDIIAVEVNVDIATVDDTLITLDLDSRGIRIGPGRAIL 60  
ATAGGGAROSTPIGLGOALYTTAGGGARKSITKGPGRVYATAGGGARKRIHIGPGRFY 120  
TTAGGGARKRITMGPGRVYYTTAGGGARORTSIGOGOALYTTAGGGATTSITIGPGOVFYR 180  
TGAGGGASIRIQRGPGRAFVTI 202

0  
60  
120  
180  
240  
300  
360  
420  
480  
540  
600  
660  
720  
780  
840  
900

SEQUENCE IDENTIFICATION NO.: 21

SEQUENCE TYPE: Nucleotide

LENGTH: 368 base pairs

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Nucleotide fragment that codifies for the V3 epitopes bound by a AGGGA spacer in the MEP TAB9. Restriction sites XbaI (positions 1 to 6) and BamHI (positions 363 to 368) are introduced.

TCTAGACTCGAGAGGCATTCGTATCGGCCAGGTGGCGCAATTTAGCAACAGCTGGCGG 60  
TGGCGCACGTCAATCTACCCCTATTGGTTAGGTAGGCTCTGTATACGACTGCCGGCGG 120  
TGGTGCAGCGAAAGTATCACCAAGGGTCCAGGCCCGTCATTACGCCACCGCGGGCGG 180  
CGGTGCCCGTAAGCGTATCCACATTGGCCCAGGCCGTGCATTCTATACTACAGCAGGTGG 240  
TGGCGCACGTAAACGCATCACTATGGGTCTGGTCGCGTCTATTACACGACCGCTGGCGG 300  
CGGTGCTAGCATTGCATCCAACGCCGGCTGGCGTGCATTGTGACCATATGATAACG 360  
CGGGATCC 368

(C) DOCKET NUMBER: P-13

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (914) 723-4300  
(B) TELEFAX: (914) 723-4301  
(C) E-MAIL: HMARZULLO@LSMAG.COM

(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues  
(B) TYPE: Amino acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of Neisseria meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs